This Raw Listing contains the General Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Seed, Brian et al.

(ii) TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES AND METHODS

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Clark & Elbing LLP
(B) STREET: 585 Commercial Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109-1024

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/756,018
(B) FILING DATE: 25-NOV-96
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/661,960
(B) FILING DATE: 12-JUN-1996

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/000,213
(B) FILING DATE: 14-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Elbing, Karen Lech
(B) REGISTRATION NUMBER: 35,238
(C) REFERENCE/DOCKET NUMBER: 00786/284002

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617/723-6777
(B) TELEFAX: 617/723-8962

(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: Not Relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Thr Glu Ala Gln Thr Thr Pro Pro Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: Not Relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Thr Asn Ser Leu Glu Thr Ser Thr Gly Thr Ser Gly Pro Pro
1 5 10 15

Val Thr

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: Not Relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu Gly Pro
1 5 10 15

Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp
20 25 30

Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro
35 40

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: Not Relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe
1 5 10 15

Leu Pro Glu Thr
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: Not Relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Asp Arg Arg Gln Ala Thr Glu Phe Glu Phe Leu Asp Phe Asp Phe
1 5 10 15

Leu Pro Glu Thr
20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: Not Relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Asp Arg Arg Gln Ala Ala Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe
1 5 10 15

Leu Pro Glu Ala
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: Not Relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Arg Asp Arg Arg Gln Ala Ala Glu Phe Glu Phe Leu Asp Phe Asp Phe
1 5 10 15

Leu Pro Glu Ala
20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2287 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGCTTACCA CCATGGACTG GACCTGGAGG TTCCTCTTCT TTGTGGTGGC AGCAGCTACA 60

GGTGTCCAGT CCCAGGTGCA GCTGGTGCAG TCTGGGGCTG AGGTGAAGAA GCCTGGGTCC 120

TCGGTGAAGG TCTCCTGCAA GGCTTCTGGA GGCACCTTCA GCAGCTATGC TATCAGCTGG 180

GTGCGACAGG CCCCTGGACA AGGGCTTGAG TGGATGGGAG GGATCATCCC TATCTTTGGT 240

ACAGCAAACT ACGCACAGAA GTTCCAGGGC AGAGTCACGA TTACCGCGGA CGAATCCACG 300

AGCACAGCCT ACATGGAGCT GAGCAGCCTG AGATCTGAGG ACACGGCCGT GTATTACTGT 360

GCGAGAGATA ATGGAGCGTA TTGTAGTGGT GGTAGCTGCT ACTCGGGCTG GTTCGACCCC 420

TGGGGCCAGG GAACCCTGGT CACCGTCTCT TCAGGTGAGT ACTGAATTCT AGCTTTCTGG 480

GGCAGGCCAG GCCTGACCTT GGCTTTGGGG CAGGGAGGGG GCTAAGGTGA GGCAGGTGGC 540

GCCAGCAGGT GCACACCCAA TGCCCATGAG CCCAGACACT GGACGCTGAA CCTCGCGGAC 600

206
207 AGTTAAGAAC CCAGGGGCCT CTGCGCCTGG GCCCAGCTCT GTCCCACACC GCGGTCACAT 660
208
209 GGCACCACCT CTCTTGCAGC CTCCACCAAG GGCCCATCGG TCTTCCCCCT GGCACCCTCC 720
210
211 TCCAAGAGCA CCTCTGGGGG CACAGCGGCC CTGGGCTGCC TGGTCAAGGA CTACTTCCCC 780
212
213 GAACCGGTGA CGGTGTCGTG GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCG 840
214
215 GCTGTCCTAC AGTCCTCAGG ACTCTACTCC CTCAGCAGCG TGGTGACCGT GCCCTCCAGC 900
216
217 AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA CACCAAGGTG 960
218
219 GACAAGAAAG TTGGTGAGAG GCCAGCACAG GGAGGGAGGG TGTCTGCTGG AAGCAGGCTC 1020
220
221 AGCGCTCCTG CCTGGACGCA TCCCGGCTAT GCAGCCCCAG TCCAGGGCAG CAAGGCAGGC 1080
222
223 CCCGTCTGCC TCTTCACCCG GAGCCTCTGC CCGCCCCACT CATGCTCAGG GAGAGGGTCT 1140
224
225 TCTGGCTTTT TCCCAGGCTC TGGGCAGGCA CAGGCTAGGT GCCCCTAACC CAGGCCCTGC 1200
226
227 ACACAAAGGG GCAGGTGCTG GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC 1260
228
229 CCCTGACCTA AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT 1320
230
231 CTCCTCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT CTTGTGACAA 1380
232
233 AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCCAG GCCTCGCCCT CCAGCTCAAG 1440
234
235 GCGGGACAGG TGCCCTAGAG TAGCCTGCAT CCAGGGACAG GCCCCAGCCG GGTGCTGACA 1500
236
237 CGTCCACCTC CATCTCTTCC TCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCCTCT 1560
238
239 TCCCCCCAAA ACCCAAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGCGTGG 1620
240
241 TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG GACGGCGTGG 1680
242
243 AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA CAACAGCACG TACCGGGTGG 1740
244
245 TCAGCGTCCT CACCGTCCTG CACCAGGACT GGCTGAATGG CAAGGAGTAC AAGTGCAAGG 1800
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247 TCTCCAACAA AGCCCTCCCA GCCCCCATCG AGAAAACCAT CTCCAAAGCC AAAGGTGGGA 1860
248
249 CCCGTGGGGT GCGAGGGCCA CATGGACAGA GGCCGGCTCG GCCCACCCTC TGCCCTGAGA 1920
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251 GTGACCGCTG TACCAACCTC TGTCCTACAG GGCAGCCCCG AGAACCACAG GTGTACACCC 1980
252
253 TGCCCCCATC CCGGGATGAG CTGACCAAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG 2040
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255 GCTTCTATCC CAGCGACATC GCCGTGGAGT GGGAGAGCAA TGGGCAGCCG GAGAACAACT 2100
256
257 ACAAGACCAC GCCTCCCGTG CTGGACTCCG ACGGCTCCTT CTTCCTCTAC AGCAAGCTCA 2160
258

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/756,018*

DATE: 06/25/97
TIME: 13:17:07

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